

Christine

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/500,796A

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RAW SEQUENCE LISTING

DATE: 01/10/2005

PATENT APPLICATION: US/10/500,796A

TIME: 14:29:20

Input Set : A:\64909-02.ST25.txt

Output Set: N:\CRF4\01102005\J500796A.raw

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3 <110> APPLICANT: The Government of the United States of America, as
4     represented by the Secretary of the Department of Health and
5     Human Services, Centers for Disease Control and Prevention
6     Chang, Gwong-Jen J.
8 <120> TITLE OF INVENTION: NUCLEIC ACID VACCINES FOR PREVENTION OF FLAVIVIRUS INFECTION
10 <130> FILE REFERENCE: 6395-64909-02
12 <140> CURRENT APPLICATION NUMBER: 10/500,796A
13 <141> CURRENT FILING DATE: 2004-07-06
15 <150> PRIOR APPLICATION NUMBER: PCT/US02/10764
16 <151> PRIOR FILING DATE: 2002-04-04
18 <150> PRIOR APPLICATION NUMBER: 09/826,115
19 <151> PRIOR FILING DATE: 2001-04-04
21 <150> PRIOR APPLICATION NUMBER: 09/701,536
22 <151> PRIOR FILING DATE: 2000-11-29
24 <150> PRIOR APPLICATION NUMBER: PCT/US99/12298
25 <151> PRIOR FILING DATE: 1999-06-03
27 <150> PRIOR APPLICATION NUMBER: 60/087,908
28 <151> PRIOR FILING DATE: 1998-06-04
30 <160> NUMBER OF SEQ ID NOS: 61
32 <170> SOFTWARE: PatentIn version 3.3
34 <210> SEQ ID NO: 1
35 <211> LENGTH: 48
36 <212> TYPE: DNA
37 <213> ORGANISM: Artificial Sequence
39 <220> FEATURE:
40 <223> OTHER INFORMATION: Description of artificial sequence; note = synthetic
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45 <222> LOCATION: (1)..(48)
46 <223> OTHER INFORMATION: Amplimer 14DV389
48 <220> FEATURE:
49 <221> NAME/KEY: CDS
50 <222> LOCATION: (25)..(48)
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55                               1           5
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59 <211> LENGTH: 8
60 <212> TYPE: PRT
61 <213> ORGANISM: Artificial Sequence
63 <220> FEATURE:
64 <223> OTHER INFORMATION: Synthetic Construct

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69 1 5
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77 <220> FEATURE:
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83 <222> LOCATION: (1)..(50)
84 <223> OTHER INFORMATION: Amplimer c14DV2453
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111 1 5
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116 <212> TYPE: PRT
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133 <220> FEATURE:
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137 <220> FEATURE:
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139 <222> LOCATION: (1)..(41)
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167 1 5
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195 <222> LOCATION: (1)..(38)
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207 <220> FEATURE:
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223 ccgcatagtt aagccagtat ctgctccctg cttgtgtgtt ggaggctcgt gagtagtgcg      120
225 cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc      180
227 ttaggggttag gcgttttgcg ctgcttcgcg atgtacgggc cagatatacg cgttgacatt      240
229 gattattgac tagttattaa tagtaatcaa ttacggggtc attagttcat agcccatata      300
231 tggagttccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaacgacc      360
233 cccgccatt gagctcaata atgacgtatg ttcccatagt aacgccaata gggactttcc      420
235 attgacgtca atgggtggac tatttacggt aaactgcca cttggcagta catcaagtgt      480
237 atcatatgcc aagtacgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt      540
239 atgccagta catgacctta tgggactttc ctacttgcca gtacatctac gtattagtca      600
241 tcgctattac catggtgatg cggttttggc agtacatcaa tgggcgtgga tagcggtttg      660
243 actcacgggg atttccaagt ctccacccca ttgacgtcaa tgggagtttg ttttggcacc      720
245 aaaatcaacg ggactttcca aaatgtcgta acaactccgc cccattgacg caaatgggcg      780
247 gtaggcgtgt acggtgggag gtctatataa gcagagctct ctggctaact agagaacca      840
249 ctgcttactg gcttatcgaa attaatacga ctactatag ggagacccaa gcttggtacc      900
251 gagctcgccg ccgcc atg ggc aga aag caa aac aaa aga gga gga aat gaa      951
252 Met Gly Arg Lys Gln Asn Lys Arg Gly Gly Asn Glu
253      1      5      10
255 ggc tca atc atg tgg ctc gcg agc ttg gca gtt gtc ata gct tgt gcg      999
256 Gly Ser Ile Met Trp Leu Ala Ser Leu Ala Val Val Ile Ala Cys Ala
257      15      20      25
259 gga gcc atg aag ttg tcg aat ttc cag ggg aag ctt ttg atg acc atc      1047
260 Gly Ala Met Lys Leu Ser Asn Phe Gln Gly Lys Leu Leu Met Thr Ile
261      30      35      40
263 aac aac acg gac att gca gac gtt atc gtg att ccc acc tca aaa gga      1095
264 Asn Asn Thr Asp Ile Ala Asp Val Ile Val Ile Pro Thr Ser Lys Gly
265 45      50      55      60
267 gag aac aga tgc tgg gtc cgg gca atc gac gtc ggc tac atg tgt gag      1143
268 Glu Asn Arg Cys Trp Val Arg Ala Ile Asp Val Gly Tyr Met Cys Glu
269      65      70      75
271 gac act atc acg tac gaa tgt cct aag ctt acc atg ggc aat gat cca      1191
272 Asp Thr Ile Thr Tyr Glu Cys Pro Lys Leu Thr Met Gly Asn Asp Pro
273      80      85      90
275 gag gat gtg gat tgc tgg tgt gac aac caa gaa gtc tac gtc caa tat      1239
276 Glu Asp Val Asp Cys Trp Cys Asp Asn Gln Glu Val Tyr Val Gln Tyr
277      95      100      105
279 gga cgg tgc acg cgg acc agg cat tcc aag cga agc agg aga tcc gtg      1287
280 Gly Arg Cys Thr Arg Thr Arg His Ser Lys Arg Ser Arg Arg Ser Val
281      110      115      120
283 tcg gtc caa aca cat ggg gag agt tca cta gtg aat aaa aaa gag gct      1335
284 Ser Val Gln Thr His Gly Glu Ser Ser Leu Val Asn Lys Lys Glu Ala
285 125      130      135      140

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287	tgg	ctg	gat	tca	acg	aaa	gcc	aca	cga	tat	ctc	atg	aaa	act	gag	aac	1383
288	Trp	Leu	Asp	Ser	Thr	Lys	Ala	Thr	Arg	Tyr	Leu	Met	Lys	Thr	Glu	Asn	
289					145					150					155		
291	tgg	atc	ata	agg	aat	cct	ggc	tat	gct	ttc	ctg	gcg	gcg	gta	ctt	ggc	1431
292	Trp	Ile	Ile	Arg	Asn	Pro	Gly	Tyr	Ala	Phe	Leu	Ala	Ala	Val	Leu	Gly	
293				160					165					170			
295	tgg	atg	ctt	ggc	agt	aac	aac	ggt	caa	cgc	gtg	gta	ttt	acc	atc	ctc	1479
296	Trp	Met	Leu	Gly	Ser	Asn	Asn	Gly	Gln	Arg	Val	Val	Phe	Thr	Ile	Leu	
297			175					180					185				
299	ctg	ctg	ttg	gtc	gct	ccg	gct	tac	agt	ttt	aat	tgt	ctg	gga	atg	ggc	1527
300	Leu	Leu	Leu	Val	Ala	Pro	Ala	Tyr	Ser	Phe	Asn	Cys	Leu	Gly	Met	Gly	
301		190					195					200					
303	aat	cgt	gac	ttc	ata	gaa	gga	gcc	agt	gga	gcc	act	tgg	gtg	gac	ttg	1575
304	Asn	Arg	Asp	Phe	Ile	Glu	Gly	Ala	Ser	Gly	Ala	Thr	Trp	Val	Asp	Leu	
305	205				210					215					220		
307	gtg	ctg	gaa	gga	gat	agc	tgc	ttg	aca	atc	atg	gca	aac	gac	aaa	cca	1623
308	Val	Leu	Glu	Gly	Asp	Ser	Cys	Leu	Thr	Ile	Met	Ala	Asn	Asp	Lys	Pro	
309				225					230					235			
311	aca	ttg	gac	gtc	cgc	atg	att	aac	atc	gaa	gct	agc	caa	ctt	gct	gag	1671
312	Thr	Leu	Asp	Val	Arg	Met	Ile	Asn	Ile	Glu	Ala	Ser	Gln	Leu	Ala	Glu	
313			240					245						250			
315	gtc	aga	agt	tac	tgc	tat	cat	gct	tca	gtc	act	gac	atc	tcg	acg	gtg	1719
316	Val	Arg	Ser	Tyr	Cys	Tyr	His	Ala	Ser	Val	Thr	Asp	Ile	Ser	Thr	Val	
317		255					260						265				
319	gct	cgg	tgc	ccc	acg	act	gga	gaa	gcc	cac	aac	gag	aag	cga	gct	gat	1767
320	Ala	Arg	Cys	Pro	Thr	Thr	Gly	Glu	Ala	His	Asn	Glu	Lys	Arg	Ala	Asp	
321		270					275					280					
323	agt	agc	tat	gtg	tgc	aaa	caa	ggc	ttc	act	gac	cgt	ggg	tgg	ggc	aac	1815
324	Ser	Ser	Tyr	Val	Cys	Lys	Gln	Gly	Phe	Thr	Asp	Arg	Gly	Trp	Gly	Asn	
325	285				290					295					300		
327	gga	tgt	gga	ctt	ttc	ggg	aag	gga	agc	att	gac	aca	tgt	gca	aaa	ttc	1863
328	Gly	Cys	Gly	Leu	Phe	Gly	Lys	Gly	Ser	Ile	Asp	Thr	Cys	Ala	Lys	Phe	
329				305					310					315			
331	tcc	tgc	acc	agt	aaa	gcg	att	ggg	aga	aca	atc	cag	cca	gaa	aac	atc	1911
332	Ser	Cys	Thr	Ser	Lys	Ala	Ile	Gly	Arg	Thr	Ile	Gln	Pro	Glu	Asn	Ile	
333			320					325						330			
335	aaa	tac	gaa	gtt	ggc	att	ttt	gtg	cat	gga	acc	acc	act	tcg	gaa	aac	1959
336	Lys	Tyr	Glu	Val	Gly	Ile	Phe	Val	His	Gly	Thr	Thr	Thr	Ser	Glu	Asn	
337		335					340						345				
339	cat	ggg	aat	tat	tca	gcg	caa	gtt	ggg	gcg	tcc	cag	gcg	gca	aag	ttt	2007
340	His	Gly	Asn	Tyr	Ser	Ala	Gln	Val	Gly	Ala	Ser	Gln	Ala	Ala	Lys	Phe	
341		350				355						360					
343	aca	gta	aca	ccc	aat	gct	cct	tcg	ata	acc	ctc	aaa	ctt	ggt	gac	tac	2055
344	Thr	Val	Thr	Pro	Asn	Ala	Pro	Ser	Ile	Thr	Leu	Lys	Leu	Gly	Asp	Tyr	
345	365				370					375					380		
347	gga	gaa	gtc	aca	ctg	gac	tgt	gag	cca	agg	agt	gga	ctg	aac	act	gaa	2103
348	Gly	Glu	Val	Thr	Leu	Asp	Cys	Glu	Pro	Arg	Ser	Gly	Leu	Asn	Thr	Glu	
349				385				390						395			
351	gcg	ttt	tac	gtc	atg	acc	gtg	ggg	tca	aag	tca	ttt	ctg	gtc	cat	agg	2151

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